



SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Conti-Fine, B.M.
- (ii) TITLE OF INVENTION: PREVENTION OF EXPERIMENTAL MYASTHANIA GRAVIS
BY NASAL ADMINISTRATION OF SYNTHETIC T EPITOPE SEQUENCES
- (iii) NUMBER OF SEQUENCES: 2
- (iv) CORRESPONDENCE ADDRESS:
- (A) ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth, P.A.
 - (B) STREET: 121 South Eighth Street, 1600 TCF Tower
 - (C) CITY: Minneapolis
 - (D) STATE: MN
 - (E) COUNTRY: USA
 - (F) ZIP: 55402
- (v) COMPUTER READABLE FORM:
- (A) MEDIUM TYPE: Diskette
 - (B) COMPUTER: IBM Compatible
 - (C) OPERATING SYSTEM: Windows 95
 - (D) SOFTWARE: FastSEQ for Windows Version 2.0b
- (vi) CURRENT APPLICATION DATA:
- (A) APPLICATION NUMBER: 08/991,143
 - (B) FILING DATE: 16-DEC-1997
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
- (A) APPLICATION NUMBER:
 - (B) FILING DATE:
- (viii) ATTORNEY/AGENT INFORMATION:
- (A) NAME: Embretson, Janet E
 - (B) REGISTRATION NUMBER: 39,665
 - (C) REFERENCE/DOCKET NUMBER: 600.423US1
- (ix) TELECOMMUNICATION INFORMATION:
- (A) TELEPHONE: 612-373-6959
 - (B) TELEFAX: 612-339-3061
 - (C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1667 base pairs
 - (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

185 F2

AAGCACAGGC CACCACTCTG CCCTGGTCCA CACAAGCTCC GGTAGCCCAT GGAGCCCTGG 60
CCTCTCCTCC TGCTCTTTAG CCTTTGCTCA GCTGGCCTCG TCCTGGGCTC CGAACATGAG 120
ACCCGTCTGG TGGCAAAGCT ATTTAAAGAC TACAGCAGCG TGGTGC GGCC AGTGAAGAC 180
CACCGCCAGG TCGTGGAGGT CACCGTGGGC CTGCAGCTGA TACAGCTCAT CAATGTGGAT 240
GAAGTAAATC AGATCGTGAC AACCAATGTG CGTCTGAAAC AGCAATGGGT GGATTACAAC 300
CTAAAATGGA ATCCAGATGA CTATGGCGGT GTGAAAAAAA TTCACATTCC TTCAGAAAAG 360
ATCTGGCGCC CAGACCTTGT TCTCTATAAC AATGCAGATG GTGACTTTGC TATTGTCAAG 420
TTCACCAAAG TGCTCCTGCA GTACACTGGC CACATCACGT GGACACCTCC AGCCATCTTT 480
AAAAGCTACT GTGAGATCAT CGTCAACCCAC TTTCCCTTTG ATGAACAGAA CTGCAGCATG 540
AAGCTGGGCA CCTGGACCTA CGACGGCTCT GTCGTGGCCA TCAACCCGGA AAGCGACCAG 600
CCAGACCTGA GCAACTTCAT GGAGAGCGGG GAGTGGGTGA TCAAGGAGTC CCGGGGCTGG 660
AAGCACTCCG TGACCTATTC CTGCTGCCCC GACACCCCT ACCTGGACAT CACCTACCAC 720
TTCTCCTTCT TAACTGGCCT GGTATTCTAC CTGCCCACAG ACTCAGGGGA GAAGATGACT 840
CTGAGCATCT CTGTCTTACT GTCTTTGACT GTGTTCTTTC TGGTCATCGT GGAGCTGATC 900
CCCTCCACGT CCAGTGCTGT GCCCTTGATT GGAAAATACA TGCTGTTCAC CATGGTGTTC 960
GTCATTGCCT CCATCATCAT CACTGTGATC GTCATCAACA CACACCACCG CTCACCCAGC 1020
ACCCATGTCA TGCCCAACTG GGTGCGGAAG GTTTTTATCG ACACTATCCC AAATATCATG 1080
TTTTTCTCCA CAATGAAAAG ACCATCCAGA GAAAAGCAAG ACAAAAAGAT TTTTACAGAA 1140
GACATTGATA TCTCTGACAT TTCTGGAAAG CCAGGGCCTC CACCCATGGG CTTCCACTCT 1200
CCCCTGATCA AACACCCCGA GGTGAAAAGT GCCATCGAGG GCATCAAGTA CATCGCAGAG 1260
ACCATGAAGT CAGACCAGGA GTCTAACAAT GCGGCGGCAG AGTGGAAGTA CGTTGCAATG 1320
GTGATGGACC ACATACTCCT CGGAGTCTTC ATGCTTGTTT GCATCATCGG AACCCTAGCC 1380
GTGTTTGCAG GTCGACTCAT TGAATTAAAT CAGCAAGGAT GAGCAGAAAA TGAGCTGAGC 1440
TTAGCTCTGC CTTGGAACCT ACCAGAGCAG AGAAGGGCAG GAGAGGAAGA TTTGTCTACT 1500
TGCTCCACTC GCACCTTATCA AACGTGTTAT ATTCCATACT TATTATTGAT GATAAGATTT 1560
ACCTTTATGT AAGTTTATGG CCTTGAAGTG TTTCTATATT GCTTCTCCCT TTAGTTCTGC 1620
TGTCTCCCTG AAGAGTGAAC CCTCTTTAGT AAATGAAGT AATCACT 1667

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 457 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Glu Pro Trp Pro Leu Leu Leu Leu Phe Ser Leu Cys Ser Ala Gly
1 5 10 15
Leu Val Leu Gly Ser Glu His Glu Thr Arg Leu Val Ala Lys Leu Phe
20 25 30
Lys Asp Tyr Ser Ser Val Val Arg Pro Val Glu Asp His Arg Gln Val
35 40 45

Val Glu Val Thr Val Gly Leu Gln Leu Ile Gln Leu Ile Asn Val Asp
 50 55 60
 Glu Val Asn Gln Ile Val Thr Thr Asn Val Arg Leu Lys Gln Gln Trp
 65 70 75 80
 Val Asp Tyr Asn Leu Lys Trp Asn Pro Asp Asp Tyr Gly Gly Val Lys
 85 90 95
 Lys Ile His Ile Pro Ser Glu Lys Ile Trp Arg Pro Asp Leu Val Leu
 100 105 110
 Tyr Asn Asn Ala Asp Gly Asp Phe Ala Ile Val Lys Phe Thr Lys Val
 115 120 125
 Leu Leu Gln Tyr Thr Gly His Ile Thr Trp Thr Pro Pro Ala Ile Phe
 130 135 140
 Lys Ser Tyr Cys Glu Ile Ile Val Thr His Phe Pro Phe Asp Glu Gln
 145 150 155 160
 Asn Cys Ser Met Lys Leu Gly Thr Trp Thr Tyr Asp Gly Ser Val Val
 165 170 175
 Ala Ile Asn Pro Glu Ser Asp Gln Pro Asp Leu Ser Asn Phe Met Glu
 180 185 190
 Ser Gly Glu Trp Val Ile Lys Glu Ser Arg Gly Trp Lys His Ser Val
 195 200 205
 Thr Tyr Ser Cys Cys Pro Asp Thr Pro Tyr Leu Asp Ile Thr Tyr His
 210 215 220
 Phe Val Met Gln Arg Leu Pro Leu Tyr Phe Ile Val Asn Val Ile Ile
 225 230 235 240
 Pro Cys Leu Leu Phe Ser Phe Leu Thr Gly Leu Val Phe Tyr Leu Pro
 245 250 255
 Thr Asp Ser Gly Glu Lys Met Thr Leu Ser Ile Ser Val Leu Leu Ser
 260 265 270
 Leu Thr Val Phe Leu Leu Val Ile Val Glu Leu Ile Pro Ser Thr Ser
 275 280 285
 Ser Ala Val Pro Leu Ile Gly Lys Tyr Met Leu Phe Thr Met Val Phe
 290 295 300
 Val Ile Ala Ser Ile Ile Ile Thr Val Ile Val Ile Asn Thr His His
 305 310 315 320
 Arg Ser Pro Ser Thr His Val Met Pro Asn Trp Val Arg Lys Val Phe
 325 330 335
 Ile Asp Thr Ile Pro Asn Ile Met Phe Phe Ser Thr Met Lys Arg Pro
 340 345 350
 Ser Arg Glu Lys Gln Asp Lys Lys Ile Phe Thr Glu Asp Ile Asp Ile
 355 360 365
 Ser Asp Ile Ser Gly Lys Pro Gly Pro Pro Pro Met Gly Phe His Ser
 370 375 380
 Pro Leu Ile Lys His Pro Glu Val Lys Ser Ala Ile Glu Gly Ile Lys
 385 390 395 400
 Tyr Ile Ala Glu Thr Met Lys Ser Asp Gln Glu Ser Asn Asn Ala Ala
 405 410 415
 Ala Glu Trp Lys Tyr Val Ala Met Val Met Asp His Ile Leu Leu Gly
 420 425 430
 Val Phe Met Leu Val Cys Ile Ile Gly Thr Leu Ala Val Phe Ala Gly
 435 440 445
 Arg Leu Ile Glu Leu Asn Gln Gln Gly
 450 455

INSF27

22